

Amendments to the Specification

Paragraph at page 5, lines 5-14:

Figures 1A-1C show ~~Figure 1 shows~~ a comparison of the amino acid sequences of the gamma-tocopherol methyltransferase from soybean contig assembled from clones sah1c.pk001.k8, sgc5c.pk001.m23, and sah1c.pk004.g2 (SEQ ID NO:8), corn contig assembled from clones cr1n.pk0179.f10:fis, cs1.pk0065.f2, cta1n.pk0031.d2, p0060.coran49r, and p0103.ciaay86r (SEQ ID NO:22, the 3'-end sequence of rice clone rls72.pk0010.g3 (SEQ ID NO:24), the 5'-end sequence of clone rls72.pk0010.g3 (SEQ ID NO:26), soybean clone sah1c.pk004.g2 (SEQ ID NO:28), wheat clone wr1.pk0077.f1:fis (SEQ ID NO:30), *Synechocystis* sp. (NCBI General Identifier No. 1001725; SEQ ID NO:39), and *Arabidopsis thaliana* (NCBI General Identifier No. 4106538; SEQ ID NO:40). Dashes are used by the program to maximize the alignment.

Paragraph at page 5, lines 15-21:

Figures 2A-2C show ~~Figure 2 shows~~ a comparison of the amino acid sequences of the 4-hydroxyphenyl-pyruvate dioxygenase from catalpa clone ncs.pk0012.g1:fis (SEQ ID NO:32), soybean clone sgc5c.pk001.j9:fis (SEQ ID NO:36), wheat clone wdk4c.pk006.m9:fis (SEQ ID NO:38), *Hordeum vulgare* having NCBI General Identifier No. 3334222 (SEQ ID NO:41), *Daucus carota* having NCBI General Identifier No. 3334219 (SEQ ID NO:42), and *Arabidopsis thaliana* having NCBI General Identifier No. 3334223 (SEQ ID NO:43). Dashes are used by the program to maximize the alignment.

Paragraph at page 24, lines 7-12:

Figures 1A-1C present ~~Figure 1 presents~~ an alignment of the amino acid sequences set forth in SEQ ID NOs:8, 22, 24, 26, 28, and 30 and the *Synechocystis* sp. and *Arabidopsis thaliana* sequences (SEQ ID NO:39 and SEQ ID NO:40, respectively). The data in Table 5 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:8, 22, 24, 26, 28, and 30 and the *Synechocystis* sp. and *Arabidopsis thaliana* sequences (SEQ ID NO:39 and SEQ ID NO:40, respectively).

Paragraph at page 26, lines 13-19:

Figures 2A-2C present ~~Figure 2~~ presents an alignment of the amino acid sequences set forth in SEQ ID NOs:32, 34, 36, and 38 and the *Hordeum vulgare*, *Daucus carota*, and *Arabidopsis thaliana* sequences (SEQ ID NO:41, SEQ ID NO:42, and SEQ ID NO:43, respectively). The data in Table 8 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:18, 32, 34, 36, and 38 and the *Hordeum vulgare*, *Daucus carota*, and *Arabidopsis thaliana* sequences (SEQ ID NO:41, SEQ ID NO:42, and SEQ ID NO:43, respectively)